

**In the claims:**

1-35. (Canceled)

36. (Currently Amended) A method for targeting a target polypeptide for ubiquitin-dependent proteolysis in a eukaryotic cell, comprising:

providing in a eukaryotic cell comprising a hybrid polypeptide comprised of that comprises (i) an F-box consisting of an amino acid sequence that is encoded by a nucleotide sequence that is at least 90% identical to the nucleotide sequence in SEQ ID NO: 3 that encodes amino acids 148-192 of SEQ ID NO: 4 or to the nucleotide sequence in SEQ ID NOs: 1, 5, 7, 9 or 11 that encodes the F-box in SEQ ID NOs: 2, 6, 8, 10 or 12, respectively, an F-box and a WD40 domain, and (ii) a target polypeptide interaction domain that binds to the target polypeptide, wherein the F-box recruits the hybrid polypeptide to a Skp1/Cul 1/F-box protein (SCF) ubiquitin ligase complex, thereby targeting the target polypeptide for ubiquitin-dependent proteolysis in the eukaryotic cell.

37. (Canceled)

38. (Canceled)

39. (Currently amended) The method of claim 38 36, wherein said ubiquitin-dependent proteolysis is by the proteasome.

40. (Cancelled)

41. (Currently amended) The method of claim 36, wherein the F-box is from an F-box polypeptide selected from the group consisting of Cdc4p, Pop1p, Pop 2p, Grr1p, Met30p, HOSp, beta TrCP[[p]], and FWD1[[p]].

42. (Currently amended) The method of claim 36, wherein the F-box ~~is from an F-box polypeptide comprising~~ comprises an amino acid sequence that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence in SEQ ID NO: 3 that encodes amino acids 148-192 of SEQ ID NO: 4 or to the nucleotide sequence in SEQ ID NOs: 1, 5, 7, 9 or 11 that encodes the F-box in ~~selected from the group consisting of~~ SEQ ID Nos. 2, 4, 6, 8, 10, and 12, respectively.

43. (Currently amended) The method of claim 36, wherein the F-box ~~is from an F-box polypeptide encoded by a nucleic acid selected from the group consisting of~~ SEQ ID Nos. 1, 3, 5, 7, 9, and 11 comprises an amino acid sequence that is identical to an F-box in any of SEQ ID NOs: 2, 4, 6, 8, 10 and 12.

44. **(Canceled)** The method of claim 36, wherein the F-box is at least 95% identical to a contiguous polypeptide sequence of a polypeptide selected from the group consisting of SEQ ID Nos. 2, 4, 6, 8, 10 and 12.
45. **(Canceled)** The method of claim 36, wherein the F-box is encoded by a nucleic acid that hybridizes under stringent conditions comprising a wash step in 0.2 x SSC at 50°C to a nucleic acid selected from the group consisting of SEQ ID Nos. 1, 3, 5, 7, 9, and 11.
46. The method of claim 36, wherein the target polypeptide is targeted for proteolysis in vitro.
47. **(Currently Amended)** The method of claim 36, wherein the ~~target polypeptide is targeted for proteolysis in a eukaryotic cell~~ is a yeast cell ~~in vivo~~.
48. **(Previously presented)** The method of claim 36, wherein the target polypeptide interaction domain is selected from the group consisting of a papillomavirus E7 polypeptide, and an SV40 LTP polypeptide.
49. **(Previously presented)** The method of claim 36, wherein the target polypeptide is selected from the group consisting of a retinoblastoma polypeptide, a p107 polypeptide, IκB, Sic1p, Cln2p, E2 or beta- catenin.
- 50-56. **(Canceled)**
57. **(New)** The method of claim 42, wherein the F-box comprises amino acids 148-192 of SEQ ID NO: 4.
58. **(New)** The method of claim 42, wherein the F-box consists essentially of amino acids 148-192 of SEQ ID NO: 4.
59. **(New)** The method of claim 58, wherein the F-box consists of amino acids 148-192 of SEQ ID NO: 4.
60. **(New)** The method of claim 58, wherein the hybrid polypeptide further comprises at least one WD domain that is encoded by a nucleotide sequence that is at least 95% identical to a nucleotide sequence of SEQ ID NO: 3 encoding a WD domain in SEQ ID NO: 4.
61. **(New)** The method of claim 58, further comprising a WD domain consisting essentially of an amino acid sequence selected from the group consisting of amino acids 260-293 of SEQ ID NO: 4; amino acids 305-333 of SEQ ID NO: 4; amino acids 345-373 of SEQ ID NO: 4; amino acids 388-416 of SEQ ID NO: 4; amino acids 428-456 of SEQ ID NO: 4; amino acids 468-497 of SEQ ID NO: 4 and amino acids 518-546 of SEQ ID NO: 4.
62. **(New)** The method of claim 36, wherein the eukaryotic cell is a mammalian cell.

63. (New) The method of claim 62, wherein the mammalian cell is a human cell.

64. (New) The method of claim 58, wherein the cell is a human cell.

65. (New) A method for targeting a target polypeptide for ubiquitin-dependent proteolysis in a eukaryotic cell, comprising:

providing a eukaryotic cell comprising a hybrid polypeptide that comprises (i) a peptide that is encoded by a nucleotide sequence that is at least 90% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 5, 7, 9 and 11, and (ii) a target polypeptide interaction domain that binds to the target polypeptide, wherein the peptide recruits the hybrid polypeptide to an SCF ubiquitin ligase complex, thereby targeting the target polypeptide for ubiquitin-dependent proteolysis in the eukaryotic cell.

66. (New) The method of claim 65, wherein the hybrid polypeptide comprises a peptide that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 5, 7, 9 and 11.

67. (New) The method of claim 66, wherein the hybrid polypeptide comprises a peptide that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in SEQ ID NOs: 1 or 3.

68. (New) The method of claim 67, wherein the hybrid polypeptide comprises a peptide that is encoded by a nucleotide sequence that is at least 95% identical to the nucleotide sequence set forth in SEQ ID NO: 3 and the eukaryotic cell is a human cell.

69. (New) A method for targeting a target polypeptide for ubiquitin-dependent proteolysis in a eukaryotic cell, comprising:

providing a eukaryotic cell comprising a hybrid polypeptide that comprises (i) a peptide that is encoded by a nucleic acid that hybridizes under stringent conditions comprising a wash step in 0.2 x SSC at 50°C to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 1, 3, 5, 7, 9, and 11, and (ii) a target polypeptide interaction domain that binds to the target polypeptide, wherein the peptide recruits the hybrid polypeptide to an SCF ubiquitin ligase complex, thereby targeting the target polypeptide for ubiquitin-dependent proteolysis in the eukaryotic cell.

70. (New) The method of claim 69, wherein the hybrid polypeptide comprises an amino acid sequence that is encoded by a nucleic acid that hybridizes under stringent conditions comprising a wash step in 0.2 x SSC at 50°C to a nucleic acid comprising the nucleotide sequence set forth in SEQ ID NOs: 1 or 3.